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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO	
09/692,412	10/20/2000	David F. Bush	04983.0206.CPUS01/38-21(1	6988	
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ARNOLD & PORTER IP DOCKETING DEPARTMENT; RM 1126(b) 555 12TH STREET, N.W.			EXAMINER		
			EINSMANN, JULIET CAROLINE		
WASHINGTO	N, DC 20004-1206		ART UNIT	PAPER NUMBER	
			1634	19	
			DATE MAILED: 04/24/2002	12	

Please find below and/or attached an Office communication concerning this application or proceeding.

	Application No.	Applie	Applicant(s)				
	09/692,412	BUSH	BUSH ET AL.				
Office Action Summary	Examiner	Art Ur	nit				
	Juliet Einsmann	1634					
The MAILING DATE of this communication appears on the cover sheet with the correspondence address Period for Reply							
A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION. - Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication. - If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely. - If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication. - Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). - Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b). Status							
1) Responsive to communication(s) filed on <u>16 l</u>	November 2001 .						
2a) This action is FINAL . 2b)⊠ Th	nis action is non-fina	d.		2			
3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under <i>Ex parte Quayle</i> , 1935 C.D. 11, 453 O.G. 213. Disposition of Claims							
4)⊠ Claim(s) <u>1-7,10-12,15-17 and 27-35</u> is/are pending in the application.							
4a) Of the above claim(s) is/are withdrawn from consideration.							
5) Claim(s) is/are allowed.							
6)⊠ Claim(s) <u>1-7,10-12,15-17 and 27-35</u> is/are rejected.							
7) Claim(s) is/are objected to.							
8) Claim(s) are subject to restriction and/or election requirement.							
Application Papers							
9) The specification is objected to by the Examiner.							
10) The drawing(s) filed on is/are: a) accepted or b) objected to by the Examiner.							
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a). 11) The proposed drawing correction filed on is: a) approved b) disapproved by the Examiner.							
			the Examine				
If approved, corrected drawings are required in reply to this Office action. 12) The oath or declaration is objected to by the Examiner.							
Priority under 35 U.S.C. §§ 119 and 120							
13) Acknowledgment is made of a claim for foreign	n priority under 35 l	ISC 8 119(a)-(d) o	r (f)				
a) All b) Some * c) None of:	in priority and or oo	5.0.0.3 1 / O(a) (a) 0					
1. Certified copies of the priority document	ts have been receiv	ed					
2. Certified copies of the priority document			,				
3. Copies of the certified copies of the prio application from the International Bu	ority documents hav ureau (PCT Rule 17	e been received in th		Stage			
* See the attached detailed Office action for a list	-			annlination)			
14) Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).							
a) The translation of the foreign language pro			r 121.	*			
Attachment(s)	K						
1) Notice of References Cited (PTO-892) 2) Notice of Draftsperson's Patent Drawing Review (PTO-948) 3) Information Disclosure Statement(s) (PTO-1449) Paper No(s)	5) 🔲 1	nterview Summary (PTO-4 lotice of Informal Patent A hther:					

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DETAILED ACTION

1. The examiner examining this application has changed. Further, the art unit where this application is being examined has changed. In order to aid matching any future papers with this application, please note that the examiner is Juliet Einsmann and the proper art unit is 1634.

Election/Restrictions

2. The restriction requirement mailed 12/24/01 is hereby WITHDRAWN. Claims 1-7, 10-12, 15-17, and 27-35 are pending and are examined herein. Applicant's preliminary amendment filed 11/16/01 cancelled any claims that were previously restricted away from the instantly pending claims. Thus, the previous telephonic restriction, and applicant's objections thereto are moot (see page 7 of the paper filed 11/16/01).

Specification

3. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Claim Rejections - 35 USC § 103

- 4. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:
 - (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

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5. Claims 4, 6, 17, 29, 30, 31, 33, and 34 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cho *et al.* (Nature Genetics, 1999, 23:203-207) in view of Lai *et al.* (Genomics, 54:31-38, 1998).

Cho *et al.* teach a method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising:

- (A) screening a mapping population of Arabidopsis plants to determine the linkage of said phenotypic trait with a collection of nucleic acid molecules, wherein said nucleic acid molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of Arabidopsis;
 - (B) calculating the linkage of each of said polymorphisms to said phenotypic trait; and
- (C) identifying said genomic DNA region associated with said phenotypic trait based on its linkage to one or more of said nucleic acid molecules (p. 205, third column).

The set of polymorphisms screened by Cho *et al.* included the polymorphism instantly disclosed as Single Nucleotide Polymorphism 466799 (confirmed in Applicant's remarks filed 11/16/01, page 8). The region of genomic DNA associated with said phenotypic trait is located within 7cM region between two single nucleotide polymorphisms (SNP), thus it is about 5cM from at least one of the polymorphisms.

Cho et al. suggest the genration of denser SNP maps for Arabidopsis (p. 205), but Cho et al. do not teach a method wherein the polymorphisms are distributed throughout the genome of Arabidopsis plants at an average density of more than one polymorphism per about 100 kb.

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Lai et al. teach a high density SNP map of a portion of the human genome, wherein the map has a density of one SNP every 30 kb, and teach that such a map was generated "efficiently and rapidly" using existing methodologies (p. 34).

Thus, it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have used the methods taught by Lai et al. in order to produce a denser SNP map for use in the identification of a region of genomic DNA associated with a phenotypic trait of interest as taught by Cho et al. The ordinary practitioner would have been motivated to provide such a method by the suggestion of Cho et al. that "The generation of denser biallelic maps should allow high-throughput identification of both monogenic and polygenic traits, effectively removing the rate-limiting nature of high resolution mapping from the study of biological processes (p. 205)." The ordinary practitioner would have been further motivated by the teachings of Lai et al. that the generation of SNP-based maps can be accomplished "efficiently and rapidly" using existing methodologies.

6. Claims 1-3, 5, 10-12, 15-16, 27, and 35 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cho *et al.* in view of Lai *et al.* as applied to claims 4, 6, 17, 29, 30, 31, 33, and 34 above, and further in view of Davis *et al.* (PNAS, Vol. 96, pp. 6541-6546, May 1999).

The teachings of Cho et al. in view of Lai et al. are applied to these claims as discussed in the previous rejections.

While the methods taught by Cho et al. and Lai et al. are both directed towards use in positional cloning, Cho et al. in view of Lai et al. do not teach a method in which the region of genomic DNA is isolated. Steps (A)-(D) are inherent properties of the generation of an F2

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generation of plants as taught by Cho et al. Cho et al. generate the F2 generation from two different ecotypes of Arabidopsis wherein on ecotype has a phenotype of interest and the other ecotype lacks the phenotype of interest (p. 205).

Davis *et al.* teach methods in which positional cloning is used to localize and isolate a region of genomic DNA associated with a phenotype of interest (p. 6542).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have included a step in which the methods of Cho *et al.* in view of Lai *et al.* are used to isolate the region of genomic DNA that is associated with the phenotype. The ordinary practitioner would have been motivated to isolate the region of genomic DNA the isolation of genomic DNA of interest aids in the elucidation of the biochemical pathways that lead to a particular phenotype. For example, Davis *et al.* teach that the availability of genes in the pathway they are examining "should be instrumental in defining the synthetic defects" mutant plants (p. 6546).

7. Claims 1-7, 10-12, 15-17, and 27-35 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cho *et al.* (Nature Genetics, 1999, 23:203-207) in view of Somerville (posted to bionet.genome.arabidopsis USENET newsgroup (May 2000)).

Cho et al. teach a method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising:

(A) screening a mapping population of Arabidopsis plants to determine the linkage of said phenotypic trait with a collection of nucleic acid molecules, wherein said nucleic acid

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molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of Arabidopsis;

- (B) calculating the linkage of each of said polymorphisms to said phenotypic trait; and
- (C) identifying said genomic DNA region associated with said phenotypic trait based on its linkage to one or more of said nucleic acid molecules (p. 205, third column).

The set of polymorphisms screened by Cho *et al.* included the polymorphism instantly disclosed as Single Nucleotide Polymorphism 466799 (confirmed in Applicant's remarks filed 11/16/01, page 8). The region of genomic DNA associated with said phenotypic trait is located within 7cM region between two single nucleotide polymorphisms (SNP), thus it is about 5cM from at least one of the polymorphisms. Steps (A)-(D) are inherent properties of the generation of an F2 generation of plants as taught by Cho *et al.* Cho *et al.* generate the F2 generation from two different ecotypes of Arabidopsis wherein on ecotype has a phenotype of interest and the other ecotype lacks the phenotype of interest (p. 205).

Cho et al. suggest the generation of denser SNP maps for Arabidopsis (p. 205), but Cho et al. do not teach a method wherein the polymorphisms are distributed throughout the genome of Arabidopsis plants at an average density of more than one polymorphism per about 100 kb.

Somerville discloses the availability of a dataset that represents more than 35,000 polymorphisms in the Arabidopsis genome, and provides instructions as to how to access the database for use in "the isolation of genes in map based cloning, among other things." Single Nucleotide Polymorphism 471736 is presumed to be a member of this large set of polymorphisms.

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Thus, it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have used the denser SNP map taught by Somerville in the identification of a region of genomic DNA associated with a phenotypic trait of interest as taught by Cho *et al.* The ordinary practitioner would have been motivated to provide such a method by the suggestion of Cho *et al.* that "The generation of denser biallelic maps should allow high-throughput identification of both monogenic and polygenic traits, effectively removing the rate-limiting nature of high resolution mapping from the study of biological processes (p. 205)," and Somerville provides such a method. The ordinary practitioner would have been further motivated by the teachings of Somerville that "This is an incredible resource – no other organism has such a rich collection of polymorphisms. Obviously, this will greatly facilitate the isolation of genes by map based cloning."

Conclusion

8. No claims are allowed.

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Any inquiry concerning this communication or earlier communications from the examiner should be directed to Juliet C. Einsmann whose telephone number is (703) 306-5824. The examiner can normally be reached on Monday through Friday, from 9:00 AM until 4:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, W. Gary Jones can be reached on (703) 308-1152. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 and (703) 305-3014.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

JEFFREY FREDMAN PRIMARY EXAMINER

Juliet C. Einsmann Examiner

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April 19, 2002